

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/604,340 A
Source: 1600- EFS
Date Processed by STIC: 7-15-05

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IFW16

RAW SEQUENCE LISTING

DATE: 07/15/2005

PATENT APPLICATION: US/10/604,340A

TIME: 08:17:01

Input Set : N:\efs\10604340A_efs\RNAi_seq_ST25.txt

Output Set: N:\CRF4\07152005\J604340A.raw

3 <110> APPLICANT: Hildinger, Markus

5 <120> TITLE OF INVENTION: Decreasing gene expression in a mammalian subject in vivo

via

6 AAV-mediated RNAi expression cassette transfer

8 <130> FILE REFERENCE: 2

10 <140> CURRENT APPLICATION NUMBER: US 10/604,340A

11 <141> CURRENT FILING DATE: 2003-07-13

13 <160> NUMBER OF SEQ ID NOS: 12

15 <170> SOFTWARE: PatentIn version 3.2

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 6437

19 <212> TYPE: DNA

20 <213> ORGANISM: Artificial

22 <220> FEATURE:

23 <223> OTHER INFORMATION: sequence for recombinant adeno-associated viral vector, including

24 plasmid backbone, with AAV2 internal terminal repeats that flank

25 expression cassette; referred to as AAV2/2 CMV luciferase

28 <220> FEATURE:

29 <221> NAME/KEY: CDS

30 <222> LOCATION: (1228)..(2883)

31 <223> OTHER INFORMATION: luciferase cDNA

33 <400> SEQUENCE: 1

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40 ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac gccagattta      240
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54 ccatagtaac gccaataggg actttccatt gacgtcaatg ggtggagtat ttacggtaaa      660
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64 acgtcaatgg gagtttgttt tggcaccaaa atcaacggga ctttccaaaa tgtcgttaaca      960
66 actccgcccc attgacgcaa atgggcggta ggcgtgtacg gtgggaggtc tatataagca      1020
68 gagctggttt agtgaaccgt cagatcctgc agaagttggt cgtgaggcac tgggcaggta      1080
70 agtatcaagg ttacaagaca ggtttaagga gaccaataga aactgggctt gtcgagacag      1140
72 agaagactct tgcgtttctg ataggcacct attggtctta ctgacatcca ctttgccttt      1200
74 ctctccacag gtgtccaggc ggccgccc atg gaa gac gcc aaa aac ata aag aaa      1254

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75

Met Glu Asp Ala Lys Asn Ile Lys Lys

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80 10                               15                               20           25
82 ctg cat aag gct atg aag aga tac gcc ctg gtt cct gga aca att gct      1350
83 Leu His Lys Ala Met Lys Arg Tyr Ala Leu Val Pro Gly Thr Ile Ala
84                               30                               35           40
86 ttt aca gat gca cat atc gag gtg gac atc act tac gct gag tac ttc      1398
87 Phe Thr Asp Ala His Ile Glu Val Asp Ile Thr Tyr Ala Glu Tyr Phe
88                               45                               50           55
90 gaa atg tcc gtt cgg ttg gca gaa gct atg aaa cga tat ggg ctg aat      1446
91 Glu Met Ser Val Arg Leu Ala Glu Ala Met Lys Arg Tyr Gly Leu Asn
92                               60                               65           70
94 aca aat cac aga atc gtc gta tgc agt gaa aac tct ctt caa ttc ttt      1494
95 Thr Asn His Arg Ile Val Val Cys Ser Glu Asn Ser Leu Gln Phe Phe
96                               75                               80           85
98 atg ccg gtg ttg ggc gcg tta ttt atc gga gtt gca gtt gcg ccc gcg      1542
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100 90                               95                               100          105
102 aac gac att tat aat gaa cgt gaa ttg ctc aac agt atg ggc att tcg      1590
103 Asn Asp Ile Tyr Asn Glu Arg Glu Leu Leu Asn Ser Met Gly Ile Ser
104                               110                               115          120
106 cag cct acc gtg gtg ttc gtt tcc aaa aag ggg ttg caa aaa att ttg      1638
107 Gln Pro Thr Val Val Phe Val Ser Lys Lys Gly Leu Gln Lys Ile Leu
108                               125                               130          135
110 aac gtg caa aaa aag ctc cca atc atc caa aaa att att atc atg gat      1686
111 Asn Val Gln Lys Lys Leu Pro Ile Ile Gln Lys Ile Ile Ile Met Asp
112                               140                               145          150
114 tct aaa acg gat tac cag gga ttt cag tcg atg tac acg ttc gtc aca      1734
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118 tct cat cta cct ccc ggt ttt aat gaa tac gat ttt gtg cca gag tcc      1782
119 Ser His Leu Pro Pro Gly Phe Asn Glu Tyr Asp Phe Val Pro Glu Ser
120 170                               175                               180          185
122 ttc gat agg gac aag aca att gca ctg atc atg aac tcc tct gga tct      1830
123 Phe Asp Arg Asp Lys Thr Ile Ala Leu Ile Met Asn Ser Ser Gly Ser
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126 act ggt ctg cct aaa ggt gtc gct ctg cct cat aga act gcc tgc gtg      1878
127 Thr Gly Leu Pro Lys Gly Val Ala Leu Pro His Arg Thr Ala Cys Val
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130 aga ttc tcg cat gcc aga gat cct att ttt ggc aat caa atc att ccg      1926
131 Arg Phe Ser His Ala Arg Asp Pro Ile Phe Gly Asn Gln Ile Ile Pro
132                               220                               225          230
134 gat act gcg att tta agt gtt gtt cca ttc cat cac ggt ttt gga atg      1974
135 Asp Thr Ala Ile Leu Ser Val Val Pro Phe His His Gly Phe Gly Met
136                               235                               240          245
138 ttt act aca ctc gga tat ttg ata tgt gga ttt cga gtc gtc tta atg      2022
139 Phe Thr Thr Leu Gly Tyr Leu Ile Cys Gly Phe Arg Val Val Leu Met
140 250                               255                               260          265

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142 tat aga ttt gaa gaa gag ctg ttt ctg agg agc ctt cag gat tac aag      2070
143 Tyr Arg Phe Glu Glu Glu Leu Phe Leu Arg Ser Leu Gln Asp Tyr Lys
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146 att caa agt gcg ctg ctg gtg cca acc cta ttc tcc ttc ttc gcc aaa      2118
147 Ile Gln Ser Ala Leu Leu Val Pro Thr Leu Phe Ser Phe Phe Ala Lys
148          285          290          295
150 agc act ctg att gac aaa tac gat tta tct aat tta cac gaa att gct      2166
151 Ser Thr Leu Ile Asp Lys Tyr Asp Leu Ser Asn Leu His Glu Ile Ala
152          300          305          310
154 tct ggt ggc gct ccc ctc tct aag gaa gtc ggg gaa gcg gtt gcc aag      2214
155 Ser Gly Gly Ala Pro Leu Ser Lys Glu Val Gly Glu Ala Val Ala Lys
156          315          320          325
158 agg ttc cat ctg cca ggt atc agg caa gga tat ggg ctc act gag act      2262
159 Arg Phe His Leu Pro Gly Ile Arg Gln Gly Tyr Gly Leu Thr Glu Thr
160 330          335          340          345
162 aca tca gct att ctg att aca ccc gag ggg gat gat aaa ccg ggc gcg      2310
163 Thr Ser Ala Ile Leu Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala
164          350          355          360
166 gtc ggt aaa gtt gtt cca ttt ttt gaa gcg aag gtt gtg gat ctg gat      2358
167 Val Gly Lys Val Val Pro Phe Phe Glu Ala Lys Val Val Asp Leu Asp
168          365          370          375
170 acc ggg aaa acg ctg ggc gtt aat caa aga ggc gaa ctg tgt gtg aga      2406
171 Thr Gly Lys Thr Leu Gly Val Asn Gln Arg Gly Glu Leu Cys Val Arg
172          380          385          390
174 ggt cct atg att atg tcc ggt tat gta aac aat ccg gaa gcg acc aac      2454
175 Gly Pro Met Ile Met Ser Gly Tyr Val Asn Asn Pro Glu Ala Thr Asn
176          395          400          405
178 gcc ttg att gac aag gat gga tgg cta cat tct gga gac ata gct tac      2502
179 Ala Leu Ile Asp Lys Asp Gly Trp Leu His Ser Gly Asp Ile Ala Tyr
180 410          415          420          425
182 tgg gac gaa gac gaa cac ttc ttc atc gtt gac cgc ctg aag tct ctg      2550
183 Trp Asp Glu Asp Glu His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu
184          430          435          440
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187 Ile Lys Tyr Lys Gly Tyr Gln Val Ala Pro Ala Glu Leu Glu Ser Ile
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190 ttg ctc caa cac ccc aac atc ttc gac gca ggt gtc gca ggt ctt ccc      2646
191 Leu Leu Gln His Pro Asn Ile Phe Asp Ala Gly Val Ala Gly Leu Pro
192          460          465          470
194 gac gat gac gcc ggt gaa ctt ccc gcc gcc gtt gtt gtt ttg gag cac      2694
195 Asp Asp Asp Ala Gly Glu Leu Pro Ala Ala Val Val Val Leu Glu His
196          475          480          485
198 gga aag acg atg acg gaa aaa gag atc gtg gat tac gtc gcc agt caa      2742
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200 490          495          500          505
202 gta aca acc gcg aaa aag ttg cgc gga gga gtt gtg ttt gtg gac gaa      2790
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204          510          515          520
206 gta ccg aaa ggt ctt acc gga aaa ctc gac gca aga aaa atc aga gag      2838

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211	Ile	Leu	Ile	Lys	Ala	Lys	Lys	Gly	Gly	Lys	Ile	Ala	Val				
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306 cgtagaaaag atcaaaggat cttcttgaga tccttttttt ctgcgcgtaa tctgctgctt 5703
308 gcaaacaaaa aaaccaccgc taccagcggg ggtttgtttg ccggatcaag agctaccaac 5763
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353 Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
354 35 40 45
357 Val Asp Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
358 50 55 60
361 Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
362 65 70 75 80
365 Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
366 85 90 95
369 Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
370 100 105 110
373 Glu Leu Leu Asn Ser Met Gly Ile Ser Gln Pro Thr Val Val Phe Val
374 115 120 125
377 Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
378 130 135 140
381 Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
382 145 150 155 160
385 Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
386 165 170 175
389 Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
390 180 185 190
393 Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
394 195 200 205

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12



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